(c) a nucleotide sequence encoding a *staufen* polypeptide comprising amino acids 2 to 577 of SEQ ID NO:6; and

(d) a nucleotide sequence encoding conservative substitutions of the polypeptides encoded by any of the sequences in (a), (b) or (c).

REMARKS

Claims 4-8 and 19-25 are now in the case.

Reconsideration of this Application and entry of the foregoing amendments are requested.

A certified copy of the foreign priority application CA 2,238,656 is enclosed as required by 35 U.S.C. 119(b). Applicant believes that the conditions for granting priority are satisfied and priority is respectfully requested.

The disclosure has been amended as requested by the Examiner in compliance with 37 C.F.R. §§. 1.821 (d). In addition, page 7 has been amended to correct the clerical error for the lack of the title of the section SUMMARY OF THE INVENTION.

Pursuant to the Examiner's request, a new copy of the original specification including figures will be hand-delivered to the USPTO in the next few days.

Claims 4 and 19 have been amended in view of the Office Action and to better define what the Applicants consider their invention, as fully supported by an enabling disclosure. Additional support for deleting the word "about" in claim 4 can be found in original claim 4. Additional support for the addition of the word "acid" in claims 4 and 19 can be found throughout the disclosure.

New claim 24 which is similar to old claim 19, now introduces the recitation that the polynucleotide sequence encodes a staufen polypeptide.

New claim 25, refers to sequences encoding the polypeptides of SEQ ID NOS:2 and 6 as supported in the disclosure. Further support for claim 25 can be found at page 11, lines 4-14, at page 12, lines 21-24, at page 29, line 25 to page 30, line 2 and at page 49, lines 14-16.

REJECTION UNDER 35 U.S.C. § 101

The Examiner has rejected claims 14-8 and 19-23 under 35 U.S.C. § 101. He alleges that these claims do not satisfy the specific, substantial and credible utility requirement.

He first alleges that there is no assertion of specific and substantial utility. He believed that the use of the terms "may be" in the enumeration of utilities for the invention appearing at p. 4, line 20 to line 8, at p. 7 and at p. 69 indicates that these utilities have not been confirmed. The Examiner further justifies his conclusion, according to which additional researches are necessary to confirm the function of the invention, on the following sentence:

> "Although its precise role is still unclear, its biochemical and molecular properties strongly suggest that it is involved in mRNA transport and/or localization."

The Examiner therefore concludes that the only confirmed utility for the invention is as a research tool to determine or confirm the role of the protein that it encodes. According to him, this type of utility does not constitute "a real world utility" or a utility sufficiently practical to satisfy the "substantial" element of the utility requirement. The Examiner therefore concludes that there is no assertion of specific, substantial and credible utility.

The Examiner also concludes that no apparent or implicit specific, substantial and credible utility can be inferred from the application. He alleges that although the utility of a nucleotide sequence may be inferred from the function of the protein that it encodes, in the present case, the function of the protein encoded by the human sequences of the present invention is not confirmed. The Examiner appears to consider that the results presented in the present application which led the Applicants to conclude that the protein encoded by the identified sequences is a h*Staufen* are not credible. He indicates that the Drosophila *Staufen* and the claimed human sequences are too different to conclude that they have the same function. In this regard, he mentions the following "considerable" differences between the claimed sequences and the Drosophila sequence: 1) "mammalian *Staufen* does not

contain th first dsRNA binding domain and the long N-terminal sequence that binds to oskar protein"; 2) "the human *Staufen* contains a tubulin binding domain which is not present in Drosophila". The Examiner also alleges that Johnston *et al.* 1993, Accession No. M69111.1 teaches that there is only 53% sequence similarity between the nucleic acid encoding human *Staufen* and Drosophila *Staufen*.

Similarly, the Examiner notes that although an apparent or implicit utility can be inferred from a nucleotide sequence which can serve as a probe for identifying homologous sequences, this utility can only be inferred when the probe permits to attribute a function to the homologous sequences identified. He alleges that in the present application the function of the claimed sequences is not confirmed, so that as probes, these sequences could only serve to identify homologous sequences of undetermined function. The Examiner adds that the homology between the claimed sequences and the Drosophila sequence is so low that the use of the former as probes would not permit to determine whether the sequences that hybridize thereto are of human origin or of another origin.

The Applicants respectfully traverse the objection as follows.

Assertion of specific and substantial utility

The Applicant respectfully disagrees with the Examiner's conclusion according to which the present application does not contain "assertions of specific and substantial utility" for the following reason.

Firstly, the use of the term "may" in the enumeration of applications for the invention does not negate their qualifications as "assertions of specific and substantial utility". The « Final guidelines for determining utility of gene-related inventions » state that is not necessary that a perfect correlation exist between the asserted utility and the results presented for the utility to be acceptable: " [A] rigorous correlation need not be shown in order to establish utility" : " reasonable correlation is sufficient ". Similarly, the "Synopsis of Applications of the Revised Interim Utility Guidelines" ("Synopsis") indicates that it is not necessary that the application demonstrate without any doubt that the invention possess the asserted utility(ies),

but simply that one of these utilities be "reasonably confirmed" (p.6 of the Synopsis) [emphasis added]

Hence, the list of utilities appearing in the specification of the present application is not a wish list of unfounded applications but a list of utilities that have reasonably been confirmed by experimental results presented in the application in examples 1 to 21. The use of the term "may" simply demonstrate that the Applicant recognizes that additional researches are necessary not only to confirm with more certainty the functions of these sequences, but more particularly to more precisely determine their mode of action and discover other more fundamental utilities that they may possess.

The admission by which the Applicants recognize that additional researches are necessary to better understand the mode of action and function of h*Staufen* does not negate its utility as was recognized by the caselaw and the USPTO:

> "[D]evelopment of a product to the extent that it is presently commercially salable in the marketplace is not required to establish usefulness within the meaning of §101." (In re Langer, 503 f. 2d 1380, 1393, 183 USPQ 288, 298 (CCPA 1974). Cited in the Federal Register vol. 66, No. 4 p. 1094).

Any discovery always constitutes a useful new point of departure for additional research:

> "As long as one specific substantial and credible use is disclosed and the statutory requirements are met, the USPTO is not authorized to withhold the patent until another, or better use is discovered. The researchers may discover higher, better or more practical uses, but they are advantaged by the starting point that the original disclosure provides." (Federal Register vol. 66, No. 4 p. 1094, in response to comment 7)

Finally, the disclosure of a single utility is sufficient to satisfy the utility requirement:

> "The patentee is required to disclose only one utility, that is, teach others how to use the invention in at least one way. The patentee is not required to disclose all possible uses, but promoting the subsequent discovery of other uses is one of the benefits of the patent system. When patents for genes are treated the same as for other chemicals, progress is promoted because the original inventor has the possibility to recoup research costs, because others are motivated to invent around the original patent, and because a new chemical is made available as a basis for future research". (Federal Register vol. 66, No. 4 p. 1094, in response to comment 5)

However, if the use of the terms "may be" and « it would be highly desirable » constitute artificial obstacles that could be circumvented by referring the Examiner to portions of the applications where utility assertions are made without using these expressions, let us refer the Examiner to the following passages:

> "Further, the present invention provides screening assays and methods for identifying modulators of staufen activity and especially of mammalian staufen activity. More particularly, the present invention relates to assays and methods for screening and identifying compounds which can enhance or inhibit the RNA virion incorporation ability of staufen and especially mammalian staufen. In one particular embodiment of the present invention, the screening assay for identifying modulators of staufen's incorporation ability comprises contacting cells or extracts containing staufen and a candidate compound, assaying a cellular response or biological function of staufen such as virion incorporation or RER targeting, for example, wherein the potential modulating compound is selected when the cellular response or staufen's biological activity in the presence of the candidate compound is measurably different than in the absence thereof." (p.9, lines 1-14)

> "In addition, the present invention relates to methods for treating an animal (such as a human) infected with a RNA virus, which comprises administration thereto of a composition comprising a therapeutically effective amount of *Staufen* (such as mammalian staufen)

> polypeptide, and/or staufen nucleic acid molecule, and/or modulators of staufen activity." (p.9, lines 15-22)
>
> "The invention further relates to the use of polypeptides and nucleic acid molecules encoding same of the present invention, to target molecules into virions of RNA viruses. In a particular embodiment, such targeting finds utility for example, in packaging cell lines." (p.9, lines 23-26)
>
> "The present invention further provides means to target molecules to RNA virions. In one particular embodiment, the present invention relates to such means to affect the morphogenesis of such RNA virions, thereby reducing infectivity thereof. In a particularly preferred embodiment, the present invention relates to a mammalian staufen protein which upon incorporation into HIV-1 virions significantly decreases the infectivity thereof." (p. 11, lines 21-27)

If the above is still not sufficient, the Applicants believe that the following portion of the disclosure proves without a doubt a credible, specific and substantial utility:

> "INCORPORATION OF STAUFEN INTO HIV-1 VIRIONS DECREASES THE INFECTIVITY THEREOF
>
> Whatever the particular mechanism of incorporation of hStau into HIV-1, the present invention clearly identifies a new HIV-targeting molecule. The effects of incorporated hStau on the infectivity of HIV-1 particles were investigated. hStau with pNL4.3 was overexpressed in 293T cells and a corresponding increase in hStau was found in purified virus preparations (Fig. 11A). Equal amounts of virus from pNL4.3- and pNL4.3/hStau-transfected cells were used to infect HeLa-CD4-bGal (MAGI; 19) and BF-24 (20) indicator cells. Both infectivity assays indicated that an excess amount of hStau in HIV-1 particles has a marked negative effect on virus infectivity [4- and a 6.7-fold decrease in MAGI and BF-24 assays, respectively; Fig. 4B & C]. These data further support

> the contention that hStau plays an integral role in virus assembly and can contribute to the infectious potential. " (p.65, example 20) [emphasis added].

Apparent or implied credible, specific and substantial utility

The Applicants respectfully disagree with the Examiner's conclusion that no apparent or implied utility can be deduced from the disclosure.

First, the USPTO recognizes that the function of a sequence and therefore its utility can be inferred from its homology with a sequence having a known function: "[there is] no scientific evidence that homology-based assertions of utility are inherently unbelievable or involve implausible scientific principles [...] When a patent application claiming a nucleic acid asserts a specific, substantial, and credible utility, and bases the assertion upon homology to existing nucleic acids or proteins having accepted utility, the asserted utility must be accepted by the examiner unless the Office has sufficient evidence or sound scientific reasoning to rebut the assertion" [our emphasis].

The USPTO also implicitly recognizes that there is no threshold value at which homology is considered sufficient to conclude that the compared sequences possess the same function but that "the Office will take into account both the **nature and degree** of homology " [our emphasis] (p. 1096 in response to commentary 19).

Here, the **nature** of the disclosed homology is that of binding domains for double-stranded RNA (dsRBDs) and not the entire protein sequence (see Figure 2D; example 1, p. 41). Of course, the difference in the sequence homology over an entire protein significantly increases when comparing the fly sequence to that of a human. In addition, the existing homology between the dsRBDs of the sequences of the invention and those of the fly *Staufen* is higher than that generally existing between the members of the dsRNA-binding proteins family. Example 9 of the application at p. 49 mentions this point:

> "The overall structure and relative position of the full-length and short-RBDs are well conserved and high sequence identity is found between corresponding dsRBDs. This is highly significant since an alignment of the domains found in the members of the dsRNA-binding protein family shows an average of only 29% amino acid identity to one another (St Johnston et al., 1992). In addition, domains 1 and 4 in the human sequence, which are short domains when compared to the consensus, are nevertheless highly similar to the corresponding fly sequences, even in the region that extends far beyond the N-terminal side of the consensus sequence [...]."

The Applicants believe that a person skilled in the art knowing that the dsRBDs homology between the members of the dsRNA-binding proteins family is generally of 29% would consider it reasonable to conclude that the human sequence having 4 dsRBDs having identity percentages of 66, 61, 52 and 47% with Drosophila dsRBDs known for encoding Staufen also encodes Staufen.

Furthermore, the inventors have not based their determination of the human sequences function solely on their homology with the Drosophila *Staufen*, but also on the following observations: **1)** incorporation of human sequences in HIV-1 virions correlating with HIV-1 genomic RNA encapsidation (p. 7, lines 13-15; legend of Fig. 10 at p. 17, lines 24-27; Fig. 10; p. 19, lines 18-20; Example 18, p. 62; p. 66, lines 19-22); **2)** an increase of h*Staufen* in virions when the latter is overexpressed (p. 7, lines 19-20, p. 19, lines 26-27; Example 20, p. 65, line 22 to line 10, p. 66; p. 66, lines 26-27); **3)** a dramatic decrease of HIV-1 infectivity correlated with an increase in the incorporation of h*Staufen* virions (p. 7, lines 20-21; legend of Fig. 11 at p. 18, lines 8-26; Fig. 11; p. 20, lines 1-2; Example 20, p. 65, line 22 to line 10, p. 66; p. 66, line 26 to line 1, p. 67); **4)** detection of h*Staufen* in clinical isolates of retrovirus including HIV-2, murine leukemia virus, and in non-retroviral RNA viruses such as Reovirus but not in DNA viruses (p. 7, lines 16-18; legend of Fig. 8D at p. 16, lines 10-22; Fig. 8D, p. 19, lines 21-23; p. 66, lines 23-25); **5)** binding of the proteins of the invention to double-stranded RNA and to tubulin *in vitro* (p. 8, lines 4-6; legend of Fig. 3-4 at pp. 13-14, lines 23 and ff.; Fig. 3 and 4; Examples 4 et 5 p. 44-47; Examples 10-12, p. 50-52; Example 16, pp. 55-59); and **6)** localization of

h*Staufen* in the cytoplasm in association with the rough endoplasmic reticulum implicating this protein in the targeting of RNA to its site of translation (p. 8, lines 6-9; legend of Fig. 6-7 at p. 14, lines 20 and ff.; Fig. 6-7, p. 19, lines 11-17; Examples 14-15, pp. 54-55; Example 17, pp. 59 and ff.).

The Applicant believes that the present claims satisfy the utility requirement and requests that the 35 U.S.C § 101 rejection be withdrawn.

REJECTION UNDER 35 U.S.C. § 112, FIRST PARAGRAPH

The Examiner rejects claims 4-8 and 19-23 under 35 U.S.C. § 112, first paragraph because he alleges that they do not satisfy the utility requirement.

The Applicant understands that if the utility requirement is found to be satisfied, this objection will be withdrawn.

The Applicant nevertheless wishes to respond as follows to specific comments made.

The Examiner alleges that the application does not teach how to use the invention sequences as targets in an anti-HIV-1 or anti-RNA virus strategy. The Examiner is referred to Example 20 of the application specifically showing that the incorporation of the sequences of the present invention into HIV viruses (one type of RNA virus) decreases their infectivity. This Example teaches one way of using the invention sequences as targets in an anti-RNA virus strategy.

The Examiner further indicates that the terminology "95% identical [to the identified sequences] " in claims 4 and 19 does not enable one skilled in the art to practice the invention because the application does not teach which 5% of the sequences can be changed without modifying the protein properties. Applicants respectfully submit that in view of the teachings of the present invention, a person of ordinary skill would believe that the specification is enabling.

The Examiner then rejects claim 4 as containing new matter. He alleges that SEQ ID NO: 27 filed by voluntary amendment and to which claim 4 relates constitutes new matter because it is impossible to determine that it indeed was part of the original specification and drawings. The Examiner is referred to the

sequence starting on Figure 1', line 3 CEL (for *C. elegans*) with "mqavf" and ending by "saskt" on Figure1' (cont'd).

In view of the above and foregoing, the Applicants respectfully request that the Examiner withdraws his rejection under 35 U.S.C § 112 first paragraph.

REJECTION UNDER 35 U.S.C. § 112, SECOND PARAGRAPH

Claims 4-8 and 19-23 have been rejected under 35 U.S.C.§112, second paragraph. The Examiner is of opinion that claims 4 and 19 [the Applicant believes that the Examiner's reference to claim 23 was erroneous and that he meant to refer to claim 19 which, contrarily to claim 23, does contain the language objected to] are indefinite because they refer to "isolated nucleic molecule" instead of "isolated nucleic acid molecule". These claims have been corrected accordingly. The objection relating to the lack of antecedent of the wording "isolated nucleic acid molecule" in claims 5 and 20 is rendered moot by this amendment.

The Examiner's objection to the use of the word "about" in claim 4 is rendered moot by the removal of this term in claim 4. The Examiner's objection relating to the absence of the word "to" in claim 4 (d) [The Examiner's reference to 4(b) rather than 4(d) was understood to be mistaken] is rendered moot by the amendment to claim 4.

The Examiner objected to the use of the terminology "highly string nt conditions" in claim 19. The Applicant disagrees with this objection. This terminology is widely used in the art and in issued US patents and a person skilled in the art would be able to determine what are the specific conditions that qualify as "highly stringent conditions" in the context of the present invention. In addition, the Examiner is referred to page 22 starting at line 20 to page 23, at line 21 which gives an example of "high stringency" conditions.

In view of the above and foregoing, the Examiner is requested to withdraw his rejection under 35 U.S.C. § 112, second paragraph.

REJECTION UNDER 35 U.S.C. § 102

Claim 19 was rejected under 35 U.S.C. §102. The Examiner alleges that Marra *et al.* 1997, Accession No. AA122533 ("Marra") discloses a sequence having a 99.8% similarity with the 2248-2770 portion of SEQ ID NO: 9. He alleges that the Marra sequence would therefore hybridize under stringent conditions with SEQ ID NO: 9. It is respectfully submitted that the portion of SEQ ID NO: 9 with which the Marra sequence possesses a similarity is a portion of the 3'UTR sequence, hence the non-protein coding region of staufen. In view of the amendment to claim 19, it is respectfully submitted that the 102(b) rejection by Marra has been rendered moot.

The applicants also submit that in view of the recitation "encoding a staufen polypeptide" that claim 24 is also free of Marra. SEQ ID NO:

The Examiner also alleges that Banfi *et al.* 1998, Accession No. G30939 ("Banfi") discloses a sequence which has 99.2% sequence similarity with certain portions of the sequences of claim 19. He therefore alleges that the Banfi *et al.* sequence would hybridize under stringent conditions with the claimed sequences. It is respectfully submitted that the sequence of Banfi *et al.* was accessible in GenEmbl on September 29, 1998: and thus after the filing of the priority application claimed, namely May 22, 1998. A certified copy of this priority application, Canadian Application no. 2,238,656 is enclosed herewith. The Banfi article published in Nature Genetics in 1996 to which GenEmbl, Accession No. G30939 refers did not contain this sequence. (A copy of this article is also enclosed). Thus, Banfi does not constitute prior art to the present invention.

The Applicant respectfully requests that the rejections under 35 U.S.C. §102 be withdrawn.

CONCLUSION

The rejections of the original claims are believed to have been overcome by the present remarks and the introduction of new claims. From the foregoing, further and favorable action in the form of a Notice of Allowance is believed to be next in order, and such an action is earnestly solicited.

It should be understood that claim amendments for which no explanation is established above were made for clarity purposes only and not for reasons related to statutory requirements for patentability.

Authorization is hereby given to charge deposit account no. 07-1742 for any deficiencies or overages in connection with this response.

Respectfully submitted,

GOUDREAU GAGE DUBUC

Katherine Britt

Reg. No. 48,089

Date: November 23, 2001

(514) 397-7419

Encls.: Banfi *et al.*, *Nature Genetics*.
Priority application

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE DISCLOSURE:

Underlines indicate insertions.

Paragraph beginning at page 7 line 12 has been amended as follows:

documents, the content of which is herein incorporated by reference.

SUMMARY OF THE INVENTION

The human homologue of the double-stranded RNA

Paragraph beginning at page 42, line 4 has been amended as follows:

"annealed complementary oligonucleotides 5'-AGCTTAATTAGCTGAC-3' (SEQ ID NO:12) and 5'-AGCTGTCAGCTAATTA-3' (SEQ ID NO:13). The MBP/mSTAU fusion protein, containing the full-length mStau sequence, was generated by PCR amplification with Vent DNA polymerase (New England BioLabs), using the primer pair 5'-CCTGGATCCGAAAG-TATAGCTTCTACCATTG-3' (SEQ ID NO:14) and 5'-TACATAAGCTT-CTAGATGGCCAGAAAAGGTTCAGCA-3' (SEQ ID NO:15). The resulting 1562 bp fragment was digested with HindIII and BamHI, and ligated in the pMal-c vector. The C-terminal fragment (mSTAU-C) was amplified with the primer pair 5'-GGATGAATCCTATTAGTAGACTTGCAC-3' (SEQ ID NO:16) and 5'-TACATAAGC-TTCTAGATGGCCAGAAAAGGTTCAG-CA-3' (SEQ ID NO:22), digested with HindIII and cloned in the EagI* and HndIII sites of pMal-c. EagI* was created by filling in the cohesive ends of EagI-digested pMal-c vector using the Klenow fragment of DNA polymerase I. This fusion vector was then digested with SacI and EcoRI and the resulting fragment was subcloned in the pMal-stop vector to generate the mSTAU-RBD3 construct. The mSTAU-TBD construct was prepared by PCR using the primer pair 5'-GCTCTAGATTCAAAG-TTCCCCAGGC-GCAG-3' (SEQ ID NO:17) and 5'-TTTAAGCTTCTCAGA-GGGTCTAGT-GCGAG-3' (SEQ ID NO:18); the product was digested with XbaI and HindIII and cloned in the pMal-stop vector. mSTAU-RBD2 and mSTAU-RBD1 were constructed by first amplifying a fragment using the primer pair 5'-CAATGTATAAGCCCGTGGACCC-3' (SEQ ID NO:19) and 5'-AAAAAGCTTGTGCAAGTCTACTAATAGGATTCACC-3' (SEQ ID

NO:20). The resulting product was digested with HindIII and cloned in the EagI* and HindIII sites of the pMal-stop vector. This vector was then used to purify the 398 bp PstI and HindIII fragment, which was subcloned in the pMAL-stop vector to generate the mSTAU-RBD2 construct. In the same way, the mSTAU-RBD1 vector was obtained by digestion with SmaI and StuI, followed by recircularization of the digestion product using T4 DNA ligase. The mSTAU-RBD4 was PCR amplified using the primer pair 5'-ATAGCCCGAGAGTTGTTG-3' (SEQ ID NO:21) and 5'-TACAT-AAGCTTCTAGATGGC-CAGAAAAGGTTCAGCA-3' (SEQ ID NO:22). "

Paragraph beginning at page 45, line 13 has been amended as follows:

"5'-TACATGTCGACTTCCTGCCA/GGGCTGCGGG-3' (SEQ ID NO:23) and 5'-TACAATCTAGATTATCAGCGGCCGCACCTCCCACA-CACAGAC-AT-3' (SEQ ID NO:24). The 3'-primer was synthesized with a NotI site just upstream from the stop codon allowing ligation of a NotI cassette containing either three copies of the HA-tag or the GFP sequence. The resulting fragment was cloned in Bluescript following digestion with SalI and XbaI. The KpnI/XbaI fragment was then subcloned in the pCDNA3/RSV vector (Jockers et al., 1996) and a NotI-cassette was introduced at the NotI site. For the TBD/GFP fusion protein, the TBD was PCR-amplified with oligonucleotides on each side of this region SEQ ID NO:25 (5'-TACATAAGCTTAAGCCACCATGGTCAAAGTTCC-CCAGGCGC-3' and SEQ ID NO:26 5'- TACAATC-TAGAGCGGCCGCGCTCAGAGGGTCTAGT-GCGAG-3')."

IN THE CLAIMS:

Claims 4 and 19 have been amended as follows: Underlines indicate insertions and words between [brackets] indicate deletions.

4. (Amended) An isolated nucleic acid molecule comprising a polynucleotide sequence at least 95 identical to a sequence selected from the group consisting of:

(a) a nucleotide sequ nce encoding a staufen polypeptide comprising amino acids from 1 to 577 of SEQ ID NO:6;

(b) a nucleotide sequence encoding a staufen polypeptide comprising amino acids from [about] 82 to [about] 577 of SEQ ID NO:6;

(c) a nucleotide sequence encoding a staufen polypeptide comprising amino acids from [about] 2 to [about] 577 of SEQ ID NO:6;

(d) a nucleotide sequence encoding a staufen polypeptide comprising amino acids from [about] 83 to [about] 577 of SEQ ID NO:6;

(e) a nucleotide sequence encoding a staufen polypeptide comprising amino acids from [about] 1 to [about] 487 of SEQ ID NO:11;

(f) a nucleotide sequence encoding a staufen polypeptide comprising amino acids from [about] 2 to [about] 487 of SEQ ID NO:11;

(g) a nucleotide sequence encoding a staufen polypeptide comprising amino acid sequence of SEQ ID NO:27; and

(h) a nucleotide sequence encoding a staufen polypeptide comprising a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f) or (g).

19. (Amended) An isolated nucleic acid molecule comprising a polynucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) SEQ ID NO:1;

(b) SEQ ID NO:3;

(c) SEQ ID NO:5;

(d) SEQ ID NO:7;

(e) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), (c) or (d) and

(f) a sequence which hybridizes under high stringency conditions to the sequence in [f] (e).